

FIGURE 1

GGCATCTGCCGAGGAGACCACGCTCCTGGAGCTCTGCTGTCTCAGGGAGACTCTGAGG
CTCTGTTGAGAATCATGCTTGGAGGCAGCTCATCTATTGCAACTGCTGGCTTGTTTC
CTCCCTTTGCCTGTCAAGATGAATAACATGGAGTCTCCACAAACCGGAGGACTACCCCC
AGACTGCAGTAAGTGTGTCAGGAGACTACAGCTTCGAGGCTACCAAGGCCCCCTGGC
CACCGGGCCCTGGCATTCCAGGAAACCAGGAAACAATGGCAACAATGGAGCCACTGGT
CATGAAGGAGCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGCTCGAGGGAGCGGG
GCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGATTCCACCAGAACATTGAGATTGCAT
TCATGGCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTT
GAGACCAACATTGAAACTCTTGATGTCATGACTGGTAGATTGGGCCCCAGTATCAGG
TGTGTATTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGACC
TTATGCACAATGGCAACACAGTCTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGAT
ACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGATGAGGTTGGCTGCGAATGGG
CAATGGCGCTCTCCATGGGACCACCAACGCTCTCCACCTTGAGGATTGCTGCTTTG
AAACTAAGTAAATATGACTAGAATAGCTCCACTTGGGAAGACTTGTAGCTGAGCTGAT
TTGTTACGATCTGAGGAACATTAAAGTTGAGGGTTTACATTGCTGTATTCAAAAATTATT
GGTTGCAATGTTGTCACGCTACAGGTACACCAATAATGTTGACAATTAGGGCTCAGAA
GAATCAACCACAAAATAGTCTCAGATGACCTTGACTAATATACTCAGCATCTTATCAC
TCTTCCTGGCACCTAAAGATAATTCTCCTTGACGCAGGTTGGAAATTTCAG
CACAGAAGTCATTGCAAAGAATTGACTACTCTGCTTTAATTAAATACCAGTTTCAGG
AACCCCTGAAGTTAAGTCATTATTCTTATAACATTGAGAGAATCGGATGTAGTGATA
TGACAGGGCTGGGCAAGAACAGGGCACTAGCTGCCTATTAGCTAATTAGTGCCTCCG
TGTCAGCTAGCCTTGACCCCTTGTATCCACAAAATACATTAAACTCTGAATT
ACATACAATGCTATTAAAGTCATAGATTAGCTATAAGTGCTTGACAGTAATGTGG
TTGTAATTGATGTTGACCTGGCTTAGATAAAACTGTGGCAAGAAAAATGTAATGAGCAATAT
AGAGAAAGATTTGACCTGGCTTAGATAAAACTGTGGCAAGAAAAATGTAATGAGCAATAT
ATGGAAATAAACACACCTTGTAAAGATAAAAAAAA

FIGURE 2

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44686
><subunit 1 of 1, 246 aa, 1 stop
><MW: 26994, pI: 6.43, NX(S/T): 0
MLWRQLIYWQLLALFFLPFCLCQDEYMEPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPGPP
GIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKEKGYPGIPPELQIAFMASL
ATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNG
NTVFSMYSYEMKGKSDTSSNHAVLKLAGDEVWLWLMNGALHGDHQRFSTFAGFLLFETK
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Important features of the protein:

Signal peptide:

amino acids 1-22

Motif name: C1q domain signature.

amino acids 137-167

C1q domain proteins.

amino acids 135-169, 202-221, 235-244, 57-91, 60-94, 54-88, 81-114, 78-111, 63-96, 51-84, 45-78, 48-81, 33-66, 66-99 and 42-75

FIGURE 3

GAGAGAATAGCTACAGATTCTCCATCCTCAGTCTTGCAAGGCAGACAGCTGTGCCAGCCGGG
CTCTGGCAGGCTCCTGGCAGC**ATG**GCAGTGAAGCTGGGACCCCTCCTGCTGGCCCTGGCCCT
GGGCCTGGCCCAGCCAGCCTCTGCCGCCGGAAAGCTGCTGGTGTTCCTGCTGGATGGTTTC
GCTCAGACTACATCAGTGAATGGCGCTGGAGTCATTGCCTGGTTCAAAGAGATTGTGAGC
AGGGGAGTAAAAGTGGATTACTTGACTCCAGACTCCCTAGTCTCTCGTATCCAATTATTA
TACCCATAATGACTGGCCGCCATTGTGAAGTCCATCAGATGATCGGGAACTACATGTGGGACC
CCACCACCAACAAGTCCTTGACATTGGCGTCAACAAAGACAGCCTAATGCCTCTGGTGG
AATGGATCAGAACCTCTGTGGGTCACTCTGACCAAGGCCAAAGGAAGGTCTACATGTACTA
CTGGCCAGGCTGTGAGGTTGAGATTCTGGGTGTCAGACCCACCTACTGCCTAGAATATAAAA
ATGTCCCACGGATATCAATTTCGCAATGCAGTCAGCGATGCTCTTGACTCCTCAAGAGT
GGCCGGGCCGACCTGGCAGCCATATACCATGAGCGCATTGACGTGGAAGGCCACCACTACGG
GCCTGCATCTCCGCAGAGGAAAGATGCCCTCAAGGCTGTAGACACTGTCCCTGAAGTACATGA
CCAAGTGGATCCAGGAGCGGGGCTGCAGGACCGCCTGAACGTCAATTATTCGGATCAC
GGAATGACCGACATTCTGGATGGACAAAGTGAATTGAGCTGAATAAGTACATCAGCCTGAA
TGACCTGCAGCAAGTGAAGGACCGCGGGCCTGTTGTGAGCCTTGGCCGCCCTGGAAAC
ACTCTGAGATATATAACAAACTGAGCACAGTGGAACACATGACTGTCTACGAGAAAGAAC
ATCCCAAGCAGGTTCTATTACAAGAAAGGAAAGTTGTCTCCTTGACTTAGTGGCTGA
TGAAGGCTGGTTCATAACTGAGAACATCGAGAGATGCTCCGTTGGATGAACAGCACCGGCA
GGCGGGAAAGGTTGGCAGCGTGGATGGCACGGCTACGACAACGAGCTCATGGACATGCGGGC
ATCTTCTGGCCTTCGGACCTGATTCAAATCCAACCTCAGAGCTGCTCCTATCAGGTCGGT
GGACGTCTACAATGTCATGTGCAATGTGGTGGCATACCCCCGCTGCCAACAACGGATCCT
GGTCCAGGGTGTGCTGAAGGGCCGCCGGCACTGCCCGCCTGTCTGGCCAGC
CACTGTGCCCTGGCACTGATTCTCTTGCA**TAA**CTGATCATATTGCTGTCTC
AGAAAAAAACACCATCAGCAAAGTGGCCTCCAAAGCCAGATGATTTCAATTATGTGTGA
ATAATAGCTTCATTAACACAATCAAGACCAGCACATTGTAATACATTATTCTGGATAAT
TCTATACATAAAAGTTCTACTTGTAAA

FIGURE 4

MAVKLGTLALALGLAQPASARRKLLVFLLDGFRSDYISDEALESLPGFKEIVSRGVKVDY
LTPDFPSLSYPNYYTLMTRHCEVHQIGNYMWDPTTNKSFDIGVNKDSLMPLWWNGSEPLW
VTLTKAKRKVYMYWPGEVEILGVRPTYCLEYKNVPTDINFANAVSDALDSFKSGRADLAA
IYHERIDVEGHHYGPASPQRKDALKAVDTVLKYMTKWIQERGLQDRLNVII FSDHGMTDIFW
MDKVIENKYISLNLDLQQVKDRGPVVSLWPAPGKHSEIYNKLSTVEHMTVYEKEAIPSRFYY
KKGKFVSPPLTLVADEGWFITENREMLPFWMNSTGRREGWQRGWHGYDNELMDMRGIFLAFGP
DFKSNFRAAPIRSVDVYNVMCNVVGITPLPNNGSWRVMCMLKGAGTAPPWPSHCALALI
LLFLLA

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 100-104, 118-122, 341-345, 404-408

N-myristoylation sites.

amino acids 148-154, 365-371

Amidation site.

amino acids 343-347

FIGURE 5

GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCGCTGCCGCCACCATGACGCTCCTCC
CCGGCCTCCTGTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGG
GGGCACCCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACGTGCCCTCGGCCA
GGCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGCAGGCTTGCCTGTAGCCCTGG
TGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAG
TGCCCCGGTGTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACC
CTGGAGATAACCGTGTGGACACGGATGAGGACCGCTATCCACAGAACGCTGGCCTTCGCCGAGT
GCCTGTGCAGAGGCTGTATCGATGCACGGACGGCCGCGAGACAGCTGCGCTCAACTCCGTG
CGGCTGCTCCAGAGCCTGCTGGCTGCGCCGCCCTGCTCCCGCACGGCTCGGGCT
CCCCACACCTGGGCCTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTGGCTGCACCT
GCGTGTGCCCGTTCATGACCGCCGAGGCCGTGGGCCCCTAGACTGGACACGTGTGC
TCCCCAGAGGCACCCCTATTATGTGTATTATTGTATTATGCCTCCCCAACACT
ACCCTGGGTCTGGCATTCCCCGTGTCTGGAGGACAGCCCCCCTGTTCTCCTCATCTC
CAGCCTCAGTAGTTGGGGTAGAAGGAGCTCAGCACCTCTCCAGCCCTAAAGCTGCAGAA
AAGGTGTACACGGCTGCCGTACCTGGCTCCCTGCTCCGGCTCCCTACCC
TCACTGGCCTCAGGCCCGCAGGCTGCCTTCCAAACCTCTGGAAAGTACCCCTGTTCT
TAAACAATTATTAAGTGTACGTGTATTAAACTGATGAACACATCCCCAAAA

FIGURE 6

MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPPLLARGAKWGQAL
PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRYPQKL
AFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHTEFIHVP
VGCTCVLPRSV

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 112-121

N-myristoylation sites.

amino acids 32-38, 55-61, 133-139

Leucine zipper pattern.

amino acids 3-25

Homologous region to IL-17.

amino acids 99-195

FIGURE 7

CGGCCAGGGCGCCGACAGCCGACCTCACCAAGGAGAACATGCAGCTGGCACTGGGCTCCTG
CTGGCCGCGTCCTGAGCCTGCAGCTGGCTGCAGCCGAAGCCATATGGTGTACCAGTCAC
GGGCTTCGGAGGGTGCCTCCCAGGATCCAGATGCCTGAGGGACTCCACCCACTGTGTCACCA
CTGCCACCCGGGTCCAGCAACACCGAGGATTGCCTCTGGTCACCAAGATGTGCCACATA
GGCTGCCCGATATCCCCAGCCTGGCCTGGGCCCTACGTATCCATCGCTTGCTGCCAGAC
CAGCCTCTGCAACCATGACTTGACGGCTGCCCTCCAGGCCCCGGACGCTCAGCCCCCAC
AGCCCCCACAGCCTGGCGCCAGGGCTCACGGCCGCCCTCCCTGAGACTGGCCAGCCCACC
TCTCCCGGCCTCTGCAGCCACCGTCCAGCACCGCTTGCCTAGGGAAGTCCTGCGTGGAGTC
TTGCCTCAATCTGCTGCCGTCCAAGCCTGGGCCCATCGTGCCTGCCGCCCTCAGGTCCC
GACCTCCCCACAATAAAATGTGATTGGATCGTGTGGTACAAAAAAAAAAAAAAA
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FIGURE 8

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77623
><subunit 1 of 1, 97 aa, 1 stop
><MW: 10160, pI: 6.56, NX(S/T): 0
MQLGTGLLIAAVLSIQLAAAEAIWCHQCTGFGGCSHGSRCLRDSTHCVTTATRVLSNTEDLP
LVTKMCHIGCPDIPSLGLGPYVSIACCQTSLCNHD
```

Important features of the protein:

Signal peptide:

amino acids 1-20

N-myristoylation sites.

amino acids 6-11 and 33-38

Prokaryotic membrane lipoprotein lipid attachment sites.

amino acids 24-34 and 78-88

FIGURE 9

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTCAAGAGGCCGGGAAGAGAAGCAAAG
CGCAACGGTGTGGTCCAAGCCGGGCTTCGCTCGCCTCTAGGACATACACGGGACCCCCCT
AACTTCAGTCCCCAAACGCACCCCTCGAAGTCTGAACTCCAGCCCCGACATCCACCGCG
CGGCACAGGCCGGCAGGCCAGGTCCCGCGAAGGCAGTGCGCAGGGGGTCGGGCAG
CTGGGCTCGGGCGGGAGTAGGGCCCCCGAGGGAGGCAGGGAGGCAGGGCTGCATATTCAAGAGTC
CGGGGCTGCGCCCTGGGCAGAGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCG
CCGCGATGAGGCCGCGTGGTCTCGCTGCTGCTGGGCCGCCGCTGCTCTGCCACGGAGCC
TTCTGCCGCCGCGTGGTCAAGGCCAAAAGGTGTGTTGCTGACTCAAGCATCCCTGCTA
AAAAATGGCCTACTTCCATGAACGTCCAGCCGAGTGAGCTTCAGGAGGCACGCCCTGGCTT
GTGAGAGTGAGGGAGGAGTCCTCAGCCTTGAGAATGAAGCAGAACAGAACAGTAATAGAG
AGCATGTTGAAAACCTGACAAAACCCGGACAGGGATTCTGATGGTGAATTCTGGATAGG
GCTTTGGAGGAATGGAGATGGGAAACATCTGGTGCCTGCCAGATCTCTACCAGTGGCTG
ATGGAAGCAATTCCCAGTACCGAAACTGGTACACAGATGAACCTTCTGCCAGTGAAGTAAAAG
TGTGTTGTGATGTATACCAACCAACTGCCAATCTGGCCTTGGGGTCCCTACCTTACCA
GTGGAATGATGACAGGTGTAACATGAAGCACAATTATATTGCAAGTATGAACCAGAGATTA
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GTGGTGTACTGAAGCAGGTATAATTCCAATCTAATTATGTTGTTATACCAACAAATACC
CCTGCTCTACTGATACTGGTTGCTTGGAACCTGTTCCAGATGCTGCATAAAAGTA
AAGGAAGAACAAAAACTAGTCCAAACCAGTCTACACTGTGGATTCAAAGAGTACCAAGAAAA
GAAAGTGGCATGGAAGTATAATAACTCATTGACTTGGTCCAGAATTGTAATTCTGGATC
TGTATAAGGAATGGCATCAGAACAAATAGCTTGGAAATGGCTGAAATCACAAAGGATCTGCAA
GATGAACTGTAAGCTCCCCCTGAGGCAAATTAAAGTAATTGTTATATGCTATTATTC
ATTAAAGAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTGCTAAAGGATGCAC
CCAAACTTCAAACCTCAAGCAAATGGACAATGCAGATAAGTTGTTATCAACACGTC
GGGAGTATGTGTTAGAAGCAATTCTTATTCTTACCTTCATAAGTTGTTATCTA
GTCATGTAATGTATATTGTTAGAATTACAGTGTGCAAAAGTATTGCTTACCTTGCATAA
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GCTCTTGTATAAAGAAACTTATTACTGTTGTCACTGAATTACACACACAAATATAG
TACCATAGAAAAGTTGTTCTGAAATAATTCTGAACTTCTGCTCTGCTTGGTCA
ATGCTAGGAAATCTCTCAGAAATAAGAAGCTATTCTTACCTAAGTGTGATATAAACCTCCTC
AAACATTTACTTAGAGGCAAGGATTGTCTAATTCAATTGTCAGAACATGTGGTCCCTCTC
TTGCCCACTAAACAAAGATGGTGTGCTGGGATTGACACTGGAGGCAGATAGTTGC
AAAGTTAGTCTAACGGTTCCCTAGCTGTATTAGCCTCTGACTATTAGTATAACAAAGAGG
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ATTAGGAAGGAAAGGAACCTACGAAATCGTGTGAAAATGGTGGCTGAAATCAATGTGGTCCCTCTC
CATATTCAATTGATGAGGGTTGCTTGAGATAGAAAATGGTGGCTCCTTCTGCTTATCTC
TAGTTCTCAATGCTTACGCCCTGTTCTCAAGAGAACAGTGTAACTCTGGTCTTCA
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FIGURE 10

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA79230
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SEGGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDFWIGLWRNGDGQTSGACPDLYQWSDG
SNSQYRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINP
TAPVEKPYLTNQPGDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSKG
RTKTSPNQSTLWISKSTRKESGMEV
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Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 214-235

N-glycosylation sites.

amino acids 86-89 and 255-258

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 266-269

N-myristoylation sites.

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145
and 212-217

FIGURE 11

GGAGA**ATGG**GAGAGCAGT GAGAGTGGAGTCGGGGTCTGGTCGGGTGGTCTGTCCTGGCATGCCCTG
CCACAGCCACTGGGCCGAAGTTGCTCAGCCTGAAGTAGACACCACCTGGGTGCGAGGCCAGGTGG
GCGTGAAGGCACAGACGCCCTGTGAATGTCCTTCTGGGCATTCCATTGCCAGCCACTGGCCCTGACC
GGTTCTCAGCCCCACACCCAGCACGCCCTGGGAGGGTGTGCGGATGCCAGCACTGCCCAATGTGCCTAC
AAGACGTGGAGAGCATGAACAGCAGCAGATTGTCCTCAACGGAAAACAGCAGATCTCTCCGTTAGAGGACT
GCCTGGTCCTCAACGTCTAGCCCAGCTGAGGTCCCCCGAGGGTCCGGTAGGCCGGTATGGTATGGTCCATG
GAGGCCTCTGATAACTGGCCTGCCACCTCTACGATGGATCAGCTCTGGCTGCCATGGGATGTGGTGTGG
TTACAGTCCAGTACCGCCTGGGTCTGGCTCTCAGCACTGGAGATGAGCATGCCCTGGCAACCAGGGCT
TCCTAGATGTGGTAGCTGCTTGCCTGGGTCAAGAAAACATGCCCTTCGGGGTACCTCAACTGTGTCA
CTGCTTTGGGATCTGCCGGTGGAGCATCATCTCTGGCTGGTCTGCCAGTGGCTGCAGGGCTTCC
ACAGAGCCATCACACAGAGTGGGTATCACCAACCCAGGGATCATCGACTCTCACCTGGCCCTAGCTCAGA
AAATCGAAACACCTTGGCCTGCAGCTCCAGCTCCCAGCTGAGATGGTGAGTCCTCAGCAGAAAGAAGGAG
AAGAGCTGGCCTTAGCAAGAACGCTGAAAATACTATCTATCCTCTCACCGTTGATGGCACTGTCTCCCCAAA
GCCCAAGGAACCTCTGAAGGAGAAGCCCTTCACTCTGTGCCCTCCTCATGGGTGTCAACAACCATGAGTTCA
GCTGGCTCATCCCCAGGGCTGGGTCTCTGGATACAATGGAGCAGATGAGCCGGAGGACATGCTGGCCATCT
CAACACCCGCTTGACCACTCTGGATGTGCCCTGAGATGATGCCACCGTCATAGATGAATACCTAGGAAGCA
ACTCGGACGACAAGCAAATGCCAGGCCTCAGGAATTCTGGTGACGTATTCAATGTTCCACCGTCA
GTTTTCAAGATACCTTCGAGATTCTGGAGCCCTGTCTTTCTATGAGTTCAGCATGCCACCCAGTTCTTTG
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TGGACGAGAGCTCCGCTGGCTTCCAGAGGCCACAGAGGAGGAGAACGAGCTAACGCTTACCATGATGGCC
AGTGGACCCACTTGCCGGACAGGGGACCCAATAGCAAGGCTCGCTCCTGGCCCAATTCAACCAGGC
AAACAATATCTGGAGATCAACCCAGTGCCACGGCCGGACAGAAGTTCAGGGAGGCTGGATGCACTGTGGTCA
AGACGCTCCCAGCAAGATAAACAGTGGCACCAAGCAGAAGAACAGGAAGGCCAGGAGACCT**TGAGGCC**
AGGCCTGAACCTCTTGCTGGGAAACCAACTCTCAAGTGGTGCAAGTCCCAGCAGGCCAGCCCCCTCTC
CCCCCTGCTGAGACTTAATCTCCACCAGCCCTAAAGTGTGGCCCTCTGTACTGGAGTTATGCTCTTTGAA
ATGTCACAAGGCCCTCCACCTCTGGGCATTGTACAAGTTCTCCCTCTGAAGTGCCTTCTGCTTT
CTTGTGGTAGGTTCTAGCACATTCTCTAGCTTCTGGAGGACTCACTCCCCAGGAAGCCTCCCTGCCTTCTC
TGGGTGTGGGGCCCCGAGTCTGGTCCATTAGAGCACAGTCCACCCAGGCTAGCACCGTGTGTCTGTCT
CCCCCTCAGAGGAGCTCTCAAATGGGATTAGCTAACCCACTCTGTCAACCCACACCAGGATGGGTGGGA
CCTGGAGCTAGGGGGTTTGCTGAGTGAGTGAGTGAACACAGAAATGGGAGTGGCAGCTGCTGAACCTGAAC
CCAGAGCCTTCAGGTGCAAAGCCATACTCAGGCCACCGACATTGTCCACCCCTGGCAGAAGGGTGCATGCC
AATGGCAGAGACCTGGGATGGGAGAGTCTGGGCGCAGGGGATCCAGCCTAGAGCAGACCTAGGCCCTGAC
TAAGGCCTCAGACTAGGGCGGGAGGGTCTCTCTCTGCTGCCAGTCCTGGCCCTGACAAGACAACAGA
ATCCATCAGGGCCATGAGTGTACCCAGACCTGACCCCTCACCAATTCCAGCCCTGACCCCTCAGGACGCTGGATG
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GACCTGCAGCCCTCCATGCCCTGCCCTCCCCACCCCCCTGGGCTCTGTGCGGCCGGAGCCTCCCAAGGAG
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CTGGCAGGAGCTCCACCTGCTGCCCTAGTGGATCCACTGGGTGAAGCCAGCTGGGCTCTGAGTCTGGTGG
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TGTAACACACCAATCAGCACCCCTGTGCTAGCTCAGTGGTGAATGCACCAATCCACACTCTGTATCTGGCT
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TTGTGTCTAGCTCAGGGATCGTAAACGCACCAATCAGCACCCCTGTCAAAACAGACCAACTTGACTCTGTAAAAT
GGACCAATCAGCAGGATGTGGGTGGGGAGACAGAGAATAAAAGCAGGCTGCCAGGCCAGTGACAAACCC
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FIGURE 12

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA79862
><subunit 1 of 1, 571 aa, 1 stop
><MW: 62282, pI: 5.56, NX(S/T): 1
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LVINVYSPAEV PAGSGRPVMVVHGGALITGAATSYDGSLAAAYGDVVVVTVQYRLGVLGFF
STGDEHAPGNQGFLDVVAALRWVQENIAPIFGDLNCVTVFAGGSAGGSIISGLVLSPVAAGLF
HRAITQSGVITTPGIIDSHPWPLAQKIANTLACSSSSPAEMVQCLQQKEGEELVLSKKLKNT
IYPLTVGTVFPKSPKELLKEKPFHSVPFLMGVNNHEFSWLIPRGWGLLDTMEQMSREDMA
ISTPVLTSDLVPPEMMPTVIDEYLGSNSDAQAKCQAFQEFMGDVFINVPTVSFSRYLRDSGS
PVFFYEFQHRPSSFAKIKPAWKADHGAEGAFVFGGPFLMDESSRLAFPEATEEEKQLSLTM
MAQWTHFARTGDPNSKALPPWPQFNQAEQYLEINPVPRAGQKFREAWMQFWSETLPSKIQQW
HQKQKNRKAQEDL
```

Important features of the protein:

Signal peptide:

amino acids 1-27

Transmembrane domain:

amino acids 226-245

N-glycosylation site.

amino acids 105-109

N-myristoylation sites.

amino acids 10-16, 49-55, 62-68, 86-92, 150-156, 155-161,
162-168, 217-223, 227-233, 228-234, 232-238, 262-268, 357-363,
461-467

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 12-23

Carboxylesterases type-B serine active site.

amino acids 216-232

FIGURE 13

CATGGAGCCTCTGCAGCTTACCGCTAAATGTTCCGGGCCAGAGCAAAGGTATTGCAG
TTTGCTGTCTATAAGTCTATGCACAGTAACGCTATTCTTCTACAACATAAAATTCTCAAA
CCTAAAATCAACAGCTTATGCCTTGAAGTGAAGGATGAAAAGGAAGAACTGTTCTCT
GGAAAAGTATAAAGGCAAAGTTCACTAGTTGAAACGTGGCCAGTGACTGCCAActCACAG
ACAGAAATTACTTAGGGCTGAAGGAAC TGACAAAGAGTTGGACCATCCCAC TTCA CGGTG
TTGGCTTTCCCTGCAATCAGTTGGAGAAC TCGGAGCCCCGCCAAGCAAGGAAGTAGAATC
TTTGCAAGAAAAAACTACGGAGTAAC TTTCCCATCTTCCACAAGATTAAGATTCTAGGAT
CTGAAGGAGAACCTGCATTTAGATTCTTGTGATTCTCAAAGAAGGAACCAAGGTGGAAT
TTTGGAAAGTATCTGTCAACCCCTGAGGGTCAAGTTGAAAGTTCTGGAGGCCAGAGGAGCC
CATTGAAGTCATCAGGCCTGACATAGCAGCTGGTTAGACAAGTGATCATAAAAAGAAAG
AGGATCTATGAGAATGCCATTGCGTTCTAATAGAACAGAGAAATGTCTCCATGAGGGTTG
GTCTCATTAAACATTTTTGGAGACAGTGTCTCACTCTGTCACCCAGGCTGGAGTG
CAGTAGTGC GTTCTCAGCTCATTGCAACCTCTGCCTTTAACATGCTATTAAATGTGGCA
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GGATTCAAGAGCACTGTGTATGACTGAAATTCTGGAATAACTGTAATGGTTATGTTAATG
GAATAAAACACAAATGTTGAAAATGTAAAATATATACATAGATTCAAATCCTTATATAT
GTATGCTTGTGTTGTACAGGATTTGTTCTTTAAGTACAGGTTCTAGTGT
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FIGURE 14

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><subunit 1 of 1, 209 aa, 1 stop
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EKYKGKVSLVVNVASDCQLTDRNYLGLKELHKEFGPSHFSVLAFCNCQFGESEPRPSKEVES
FARKNYGVTFPIFHKIKILGSEGEPAFRFLVDSSKKEPRWNFWKYLVNPEGQVVKFWRPEEP
IEVIRPDIAALVRQVIKKKEDL
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Important features of the protein:

Signal peptide:

amino acids 1-31

Glutathione peroxidases signature 2.

amino acids 104-112

Glutathione peroxidases.

amino acids 57-82

FIGURE 15

TGTCGCCTGGCCCTGCC**ATG**CAGACCCCGCAGCGTCCCCTCCCCGCCCTCTGCTTCTGCTGCTGCTA
CTGGGGGGCGCCCACGGCTTCTTGAGGAGCCGCCGCTTAGCGTGGCCCCCAGGGACTACCTGAACCAC
TATCCCGTGTGTTGTGGGAGCGGGCCCGACGCCCTGACCCCGCAGAAGGTGCTGACGACTCAACATCCAGCGA
GTCCTGCGGGTCAACAGGACGCTGTTATTGGGACAGGGACAACCTCTACCGCTAGAGCTGGAGCCCCACG
TCCACGGAGCTGCGGTACCAGAGGAAGCTGACCTGGAGATCTAACCCAGCGACATAACGTGTGCGATGAAG
GGCAAACAGGAGGGCGAGTGTCAAACCTCGTAAAGGTGCTGCTCCCTGGGACGAGTCCACGCTTTGTGTC
GGTCCAACGCCCTCAACCCGGTGTGCGCAACTACAGCATAGACACCCCTGAGCCCCTGGAGACAAACATCAGC
GGTATGGCCCGCTGCCGTACGACCCCAAGCACGCATGTTGCCCTTCTCTGACGGGATGCTCTCACAGCT
ACTGTTACCGACTTCTAGCATTGATGCTGTCATCTACCGCAGCCTCGGGACAGGCCACCCCTGCGCACCGTG
AAACATGACTCCAAGTGGTCAAAGAGCCTACTTGTCCATGCGGTGGAGTGGGAGCCATGTCTACTTCTTC
TTCCGGGAGATTGCGATGGAGTTAACCTGGAGAAGGTGGTGGTGTCCCGCTGGCCGAGTGTGCAAGAAC
GACGTGGGAGGCTCCCCCGCGTGTGGAGAACGAGTGGACGTCTCTGAAGGCGCGGCTCAACTGCTCTGTA
CCCCGAGACTCCCATTCTACTTCAACGTGCTGCAGGCTGTACGGCGTGGTCAGCCTCGGGGCCGGCGCGTG
GTCCTGGCGTTTTTCCACGCCAGCAACAGCATCCCTGGCTCGGCTGTGCGCCTTGACCTGACACAGGTG
GCAGCTGTGTTGAAGGGCGCTTCCGAGAGCAGAAGTCCCCGAGTCCATCTGGACGCCGGTGCAGGAGGATCAG
GTGCCGACCCCCGGGGGGTGTGCGCAGCCCCCGGATGCACTACAATGCTCCAGGCCCTGCGCGGATGAC
ATCCTCAACTTGTCAAGACCCACCCCTGTATGGACGAGGGCGGTGCCCTCGCTGGGCGATGCCCTGGATCTG
CGGACCCCTGATGAGGGCACCAGCTGACTCGAGTGGCTGTGACGTGGAGCCGGCCCTGGGCAACCCAGACCGT
GTCTTCTGGGTTCTGAGGCGGGGAGGTCTCAAGTTCTCGTCCGGCCCAATGCGCAGCACCTCAGGGACGTCT
GGGCTCAGTGTCTTCTGGAGGAGTTGAGACACTACGGGGGAGCAGGTGTGGACGGGGGGGGTGGCAGACA
GGGAGCGGCTGCTGAGCTGGAGCTGGACGCAGCTTGGGGGGCTGTGGCTGCCTCCCCGCTGCGTGGTC
CGAGTGCCTGTGGCTCGCTGCCAGCAGTACTCGGGGTGTATGAAGAACTGTATGGCAGTCAGGACCCCTACTGC
GGGTGGGCCCGACGGCTCTGCATCTCCTCAGCCGGCACAGAGCCGCTTGAGCAGGACGTGTCCGG
GCCAGCACCTCAGGCTTAGGGACTGCACAGGACTCCTCGGGGCCAGCCTCTCCGAGGACCGCGGGCTGGTG
TCGGTGAACCTGCTGGTAACGTGCTGGTGGCGGCTTCTGTGGTGGAGCGCTGGTGTCCGGCTTCAGCGTGGG
TGGTCTGTTGGCCTCCGTGAGCGGGAGCTGGCCGGCGCAAGGACAAGGAGGCCATCTGGCGCACGGGGCG
GGCAGGGCGGTGCTGAGCTCAGCCGCTGGCGAGCGCAGGGCGCAGGGTCCGGGGCGGGGGCGAGGCGGT
GGGGTGGCGCCGGGGTCCCCCGAGGCCCTGCTGGCGCCCTGATGCGAGAACGGCTGGCCAAGGCCACGCTG
CTGAGGGCGGGCCACGACCTGGACTCGGGCTGCTGCCACGCCGAGCAGGCCGCTGCCAGAACGCG
CTGCCCACTCCGCACCCGCACCCCTGGGCCCTGGGCCCTGGGACCAAGGCCACCCCTGCTCCCGGCC
TCCGCTTCATCCTCCCTCTGCTGCTGGCGCCCGCCGGCCCCGAGCAGCCCCCGCGCTGGGAGGCCAC
CCGACGGCCCGCTATGTCGCCCGCCGCCGCGCCTCCACGGGAGCTTCCGCTCACCCCCCACGCCAGC
CCGGACGGCCGGGGTGTGCTGGCGCCACGGGCCCTGGACCGCAGCCTCAGGCCGAGTGGCTCCCGCG
CCCTGGAGCCCGCCCGACGGGAGCCTGAGGAGGCCACTGGGCCCCCAGGCCACCGCGCTGCCACGCCGG
CGCACCCACACGTTAACAGCGCGAGGGCCCTGGGAGCGCAGGGCTGCCACGCCGGGACA
GACTTGGCCCACCTCCTCCCTATGGGGGGGAGCAGGAGCTGCGCCCCCGTGCCAGAACCCGGGGGGGGCAACTCCG
ATGCCCTGGCAGTGCACGCCACGGGAACCGAGGAGCAGAGACGGTGCCAGAACCCGGGGGGGGCAACTCCG
AGTGGGTGCTCAAGTCCCCCGCGACCCACCCCGGGAGTGGGGGGCCCTCCGCCACAAGGAAGCACAACAG
CTGCCCTCCCCCTACCCGGGGCGCAGGACGCTGAGACGGTTGGGGGTGGTGGCGGGAGGACTTTGCTATG
GATTGAGGTTGACCTATGCGCTAGGTTGGTTTTTGCACTTTGGTTCTTGCAGTTGGTTCTTGCAGGTTTCTAACC
AATTGCACAACCTCGTTCTGGGTGGCGCAGGAGGGAGGCTGGACGCCGGTGGGAATGGGGGCCACAG
CTGCAGACCTAACGCCCTCCCCCACCCCTGGAAAGGTCCCTCCCAACCCAGGCCCTGGCGTGTGGGTGTGCG
TGCCTGCGCTGCCGTGTCAGGGCCAGCGCTGCAAGGGGCCAGGGAGGTGGCGTGTGCGTGCAGCGAAGGCTGCTG
TGGCGCTGTGTCAGTGGGCCAGCGCTGCAAGGGAGGTGTGTCACAGCGAGCAGATCGTGGTGGGCCAGCGGCC
TGGCGTTGGCTGAGCCGACGCTGGGCTTCCAGAAGGCCGGGGCTCCGAGGTGCCGGTTAGGAGTTGAAC
CCCCCCCACCTGCAGAGGGAGCGGGACAATGCCGGGTTTCAGCAGGAGACACGAGGAGGGCTGCCGG
AGTCACATCGGCAGCAGCTGCTAAAGGGCTTGGGGCCTGGGGGGCGCGAAGGTGGTGGGGCCCTGTAA
ATACGGCCCCAGGGTGGTGGAGAGAGTCCCATGCCACCCGCTCCCTTGTGACCTCCCCCTATGACCTCCAGCTGA
CCATGCATGCCACGTGGCTGGCTGGCTGGCTGCCCTCTGCCCTTTGGAGTTGCCCTCCCCAGCCCCCTCCCCATCAAT
AAAACCTGTTACAACCAAAAAAAAAAAAAAA

FIGURE 16

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80145
><subunit 1 of 1, 888 aa, 1 stop
><MW: 95285, pI: 8.89, NX(S/T): 8

MQTPRASPPRPALLLLLLLGGAHGLFPEEPPLSVAPRDYLNHYPVFGSGPGRLTPAEGA
DDLNIRQVLRVNRTLFIGDRDNLYRVELEPPTSTELRYQRKLTWRSNPSDINVCRMKGKQEG
ECRNFVKVLLRDESTLFVCGSNAFNPVCANYSIDLQPVGDNISGMARCPYDPKHANVALF
SDGMLFTATVTDFLAIDAVIYRSILGDRPTLRTVKHDSKWFKEPYFVHAVEWGSHVYFFFREI
AMEFNYLEKVVVSRVARVCKNDVGGSPrVLEKQWTSFLKARLNCSVPGDSHFYFNVLQAVTG
VVSLGGRPVVLAVFSTPSNSIPGSAVCAFDTQVAAVFEGRFREQKSPESIWTPVPEDQVPR
PRPGCCAAPGMQYNASSALPDDILNFVKTHPLMDEAVPSLGHAPWILRTLMRHQLTRVAVDV
GAGPWGNQTVVFLGSEAGTVLKFLVRPNASTSGTGLSVFLEEFETYRPDRCGRPGGGETGQ
RLSLELDAASGGLAAFPRCVVRRPVARCQQYSGCMKNCIGSQDPYCGWAPDGSCIIFLSPG
TRAafeQDVSGASTSGLDCTGLLRASLSEDRAGLVSVNLLVTSSVAAFFVGAVVSGFSVGW
FVGLRERRELARRKDKEAILAHGAGEAVLSVSRLGERRAQGPGRGGGGGGAGVPPEALLA
PLMQNGWAKATLLQGGPHDLDGLLPTPEQTPLPQKRLPTPHPHHALGPRAWDHGHPLLPA
SASSSLLLAPARAPEQPPAPGEPTPDGRLYAARPGRASHGDFPLTPHASPDRRVVSAVTG
PLDPASAADGLPRPWSPPPTGSLRRPLGPHAPPAATLRRTHTFNSGEARPGDRHRGCHARPG
TDLAHLLPYGGADRTAPPVP
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 318-339, 598-617

N-glycosylation sites.

amino acids 74-78, 155-159, 167-171, 291-295, 386-390, 441-445,
462-466

Glycosaminoglycan attachment sites.

amino acids 51-55, 573-577

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation sites.

amino acids 21-27, 50-56, 189-195, 333-339, 382-388, 448-454,
490-496, 491-497, 508-514, 509-515, 531-537, 558-564, 569-575,
574-580, 580-586, 610-616, 643-649, 663-669, 666-672, 667-673,
668-674, 669-675, 670-676, 868-874, 879-885

FIGURE 17

AGCAACTCAAGTCATCATTGCTCTGAGAGAGAGGAGCAGCGCGTTCTCGGCCGGGACAGC
AGAACGCCAGGGGACCCTCACCTGGGCACGCCGGGGCACGGGCTTGATTGCTCTGGGTG
CGGAGACCCGCGCCTGCACGCCGGGCAACCTTGCAGTCGCGTTGGCTGCTG
CGATCGGCCGGCGGGTCCCTGCCGAAGGCTCGGCTGCTCTGTCCACCTCTTACACTTCTTC
ATTATCGGTGGATCATTGAGAGTCGTCTGTAAATGTTGGCACTTGCTACTTATT
GCTTCTTCTGGCGACAGTCCAGCAGTCGCCAGACCGGGAGAAAGGCAGCTGAGCCCG
GAGAAGAGCGAAATATGGGGACCCGGCTAAAGCAGACGTCGTCTCCGCCGCTATT
CTATATTCAAGGCAGTGGATACTCAGGAAATAATTACATCTTCCAGGCAGAGGTCT
TCCAGGTGAAAGTCTCAGCACCAAGAGGAGCAATTCACTAGAGTTGGAGTCCAGGTTAGAC
CGAAAAGATGGGTCTTCATAGTAAGATACTAGAATGTATGCAAGCTACAAAATCTGAAGGT
GGAAATTAAATTCCAAGGGCAACATGTGGCAAATCCCCATATATTTAAAAGGGCCGGTT
ACCATGAGAACTGTGACTGTCCTCTGCAAGATACTGCAGCCTGGCTACGGGAGATGAACTGC
CCTGAAACCATTGCTCAGATTCAAGAGAGATCTGGCACATTCCCTGCTGTGGATCCAGAAA
GATTGCAGTAGAAATCCAAAAAGATTGGACAGAGGCAGAGCCTATGTCACTACACCTAA
AGGATAACAAGGTTATATCAAGACTCATGGTGAACATGTAGGTTTAGAATTTCATGGAT
GCCATACTACTTTCTTGACTAGAAAGGTGAAGATGCCAGATGTGGAGCTTTGTTAATT
GGGAGACTGGCTTGGAAAAAAAGAAATCCAATTCAAACATCCATCCGATCTTCCTGGT
GTGGCTCCACAGATTCCAAGGATATCGTATGCCCTACGTACGATTGACTGATTGTTCTG
GAAACCATGGCCGGTAAGTCTGGATATGATGTCCGTCAAGCTAACACGGCTCCCTG
GGAAAGCAAAATCCACTGCCGTCTGGAGAGGGCGAGACAGCCGAAAGAGAGACTCGAGC
TGGTTAAACTCAGTAGAAAACACCCAGAACTCATAGACGCTGTTCACCAACTTTCTC
TTAACACGATGAAAACCTGTATGGTCCCATTGTGAAACATATTCATTGATTCTT
CAAGCATAAGTATCAAATAATATCGATGGCACTGTAGCAGCTATGCCCTGCCATATTG
TAGTTGGTACAGTGTGTGCTGAAGCAGGATTCCATCTACTATGAACATTAAATGAG
CTGCAGCCCTGGAAACACTACATTCCAGTTAAGAGCAACCTGAGCGATCTGCTAGAAAAACT
TAAATGGCGAAAGATCACGATGAAGAGGCCAAAAGATAGCAAAAGCAGGACAAGAATTG
CAAGAAATAATCTCATGGCGATGACATATTCTGTTATTATTCAAACATTCCAGGAATAT
GCCAATTACAAGTGAGTGAGCCCCAAATCCGAGAGGGCATGAAAAGGGTAGAACACAGAC
TGAGGACGACCTCTCCCTGTACTGCCATAGGAAAAGACCAAAGATGAACTCTGATATG
CAAAATAACTCTATTAGAATAATGGTGTCTGAAGACTCTTCTTAACAAAAAGAAGAATT
TTTTAAGTATTAATTCCATGGACAATATAAAATCTGTGTGATTGTTGCAGTATGAAGACA
CATTTCTACTTATGCAGTATTCTCATGACTGTACTTAAAGTACATTGTTAGAATTTATAA
TAAAACCACCTTATTAAAGGAAAAAA

FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84917
><subunit 1 of 1, 502 aa, 1 stop
><MW: 58043, pI: 7.94, NX(S/T): 2
MFGTLLLYCFFLATVPALAETGGERQLSPEKSEIWGPGLKADVVLPARFYIQAVENTSGNKF
TSSPGEKVFQVKVSAPEEQFTRGVQVLDRKDGSFIVRYRMYASYKNLKVEIKFQGQHVAKS
PYILKGPVYHENCDCPLQDAAWLREMNCPETIAQIQRDLAHFPAVDPEKIAVEIPKRGQR
QSLCHYTLKDNKVYIKTHGEHVGFRIFMDAILLSLTRVKMPDVELFVNLDWPLEKKKSNS
NIHPIFSWCGSTDSKDIVMPTYDLTDVLETMGRVSLDMMSVQANTGPPWESKNSTAVWRGR
DSRKERLELVKLSRKHPELIDAFTNFFFFKHDENLYGPIVKHISFFDFKHKYQINIDGTV
AAYRLPYLLVGDSVVLKQDSIYYEHFYNELQPWKHYIPVKSNLSDLLEKLWAKDHDEEAKK
IAKAGQEFAARNNLMGDDIFCYYFKLFQEYANLQVSEPOIREGMKRVEPQTEDDLFPCTCHRK
TKKDEL

Important features of the protein:

Signal peptide:

amino acids 1-17

N-glycosylation sites.

amino acids 302-306, 414-418

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 243-247, 495-499

Tyrosine kinase phosphorylation site.

amino acids 341-348

N-myristoylation sites.

amino acids 59-65, 118-124, 184-190, 258-264, 370-376, 439-445

Endoplasmic reticulum targeting sequence.

amino acids 499-504

FIGURE 19

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGTGGTCCGCATCCA
GCCTAGCGTGTCCACG**A**T**G**CGGCTGGCTCCGGACTTCGCTACCTGTTGCGTAGCGATCG
AGGTGCTAGGGATCGCGTCTCCTCGGGATTCTTCCCGTCCGTTGCTCTGCC
AGAGCGAACACGGAGCGGCCAGCGCCGAACCCTCGGCTGGAGCCAGTTCAACTG
GACCACGCTGCCACCACCTCTTCAAGTAAAGGTGTTATTGTTCTGATAAGATGCCTTGAGAG
ATGATTTGTGTTGGGTCAAAGGGTGTGAAATTATGCCCTACACAACCTACCTTGGA
AAAGGAGCATCTCACAGTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCCTGAAT
CAAGGCATTGATGACGGGGAGCCTTCTGGCTTGTGACGTACAGGAAACCTCAATTCTC
CTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAAGCAGCTGGAAAAGAATAGTCTT
TATGGAGATGAAACCTGGTTAAATTATTCCAAAGCATTGTGGAATATGATGGAACAAAC
CTCATTTCGTGTCAAGATTACACAGAGGTGGATAATAATGTCAGCAGGCAATTGGATAAAG
TATTAAGAGGAGATTGGGACATATTAATCCTCACTACCTGGGCTGGACCACATTGGC
CACATTCAGGGCCCAACAGCCCCCTGATTGGCAGAAGCTGAGCAGATGGACAGCGTGCT
GATGAAGATCCACACCTCACTGCAAGGAGAGAGACGCCATTACCAATTGCTGG
TTCTTGTGGTGACCATGGCATGTCTGAAACAGGAAGTCACGGGCTCTCACCGAGGAG
GTGAATACACCTCTGATTTAATCAGTTCTGCGTTGAAAGGAAACCCGGTGATATCCGACA
TCCAAAGCACGTCCAAT**A****T****G**ACGGATGTGGCTGCGACACTGGCAGATAGCACTTGGCTTACCGA
TTCCAAAAGACAGTGTAGGGAGCCTTATTCCAGTTGTGGAAGGAAGACCAATGAGAGAG
CAGTTGAGATTTTACATTGAATAACAGTCAGCTTAGTAAACTGTTGCAAGAGAATGTGCC
GTCATATGAAAAGATCCTGGTTGAGCAGTTAAAATGTCAGAAAGATTGCATGGAACT
GGATCAGACTGTACTTGGAGGAAAAGCATTCAAGACTCTGCTTCAACCTGGCTCCAAGGTT
CTCAGGCAGTACCTGGATGCTCTGAAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCCA
GTTCTCACCTGCTCTGCTCAGCGTCCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAAGT
CCCACTGTCATCTCCTGGTTCTGCTCTTATTGGTGATCCTGGTTCTTCGGCCG
TTCACGTATTGTGTGCACCTCAGCTGAAAGTCGTGCTACTTCTGTGGCCTCTGTGGCTG
GCGGCAGGCTGCCTTCGTTACCAAGACTCTGGTGAACACCTGGTGTGCAAGTGTGG
CAGTGCCTGGACAGGGGGCTCAGGGAAAGGACGTGGAGCAGCCTTATCCCAGGCCTCTGG
TGTCCCACACAGGTGTTCACATCTGTGCTGTCAGGTCAAGTCCTCAGTTCTGGAAAGCT
AGGTTCTGCGACTGTTACCAAGGTGATTGTAAGAGCTGGCGGTACAGAGGAACAAGCCC
CCCAGCTGAGGGGGTGTGAATCGGACAGCCTCCCAGCAGAGGTGTGGAGCTGCAGCTGA
GGGAAGAAGAGACAATCGGCCCTGGACACTCAGGAGGGTCAAAGGAGACTGGTCGCACCAC
TCATCCTGCCACCCCCAGAATGCATCCTGCCTCATCAGGTCCAGATTCTTCCAAGGCGGA
CGTTTCTGTTGGAATTCTTAGTCCTTGGCCTGGACACCTTCATTGTTAGCTGGGGAGTG
GTGGTGAGGCAGTGAAGAAGAGGGGGATGGTACACTCAGATCCACAGAGGCCAGGATCAAG
GGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCCACCCAAACCCCTGCACAGCCCTCATC
CCCTCTGGCTTGAGCCGTCAAGGGCCCTGTGCTGAGTGTCTGACCGAGACACTCACAGCTT
TGTCTCATCAGGGCACAGGCTCTCGGAGCCAGGATGATCTGTGCCCCGCTGACCTCGGGC
CCATCTGGGCTCATGCTCTCTCGTATTGAATTAGTACCTAGCTGCACACAGTATGTA
GTTACCAAAAGAATAAACGGCAATAATTGAGAAAAAAA

FIGURE 20

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84920
><subunit 1 of 1, 310 aa, 1 stop
><MW: 33875, pI: 7.08, NX(S/T): 2
MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPAPAEPSAGASSNWTLPP
PLFSKVVIVLIDALRDDFVFGSKGVKFMPYTTYLVEKGASHSFVAEAKPPTVTMPRIKALMT
GSIPGFVDVIRNLNSPALLEDSVIRQAKAAGKRIVFYGDETWKLFPKHFVEYDGTSFFVS
DYTEVDNNVTRHLDKVLKRGDWLILHYLGLDHIGHISGPNSPLIGQKLSEMDSVLMKIHT
SLQSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ
```

Important features of the protein:

Signal peptide:

amino acids 1-34

Transmembrane domain:

amino acids 58-76

N-glycosylation sites.

amino acids 56-60, 194-198

N-myristoylation sites.

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,
275-281, 278-284

Amidation site.

amino acids 154-158

Cell attachment sequence.

amino acids 205-208

FIGURE 21

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCAGCTCAGCAATGGCAAT
GGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTGGGGCTGCGCTCTGCCTGACAGGGTCCC
AAGCCCTGCAGTGCTACAGTTGAGCACACCTACTTGGCCCTTGACCTCAGGGCCATG
AAGCTGCCAGCATCTCCTGTCCTCATGAGTGCTTGAGGCTATCCTGTCTGGACACCAG
GTATCGCGCGCCGGTGACCTGGTGCAGGAAGGGCTGCTGGACCGGGCTCCTGCAGGGCCAGA
CGCAATCGAACCCGGACGCGTGCCGCCAGACTACTCGGTGGTGCAGGGCTGCACAACGTGAC
AAATGCAACGCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCC
GCCGACGCTCAGCGCGCCGAGTGCTACGCCCTGTATCGGGTCCACCAGGATGACTGCGCTA
TCGGCAGGTCCCGACGAGTCCAGTGTACCGAGGACCAAGCCCTGCTTCCAGGGCAGTGGC
AGAATGACAGTTGCAATTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTG
CACCAACGAGGGCACCACCAAGCCCTGGACAGCCATCGACCTCCAGGGCTCCTGCTGTGAGG
GGTACCTCTGCAACAGGAAATCCATGACCCAGCCCTTACCAAGTGCTTCAGCCACCACCCCT
CCCCGAGCACTACAGGTCCCTGGCCCTGCTCCTCCAGTCCTCCTGCTGGTGGGCTCTCAGC
ATAGACCGCCCTCCAGGATGCTGGGACAGGGCTCACACACCTCATTCTGCTGCTTCAGC
CCCTATCACATAGCTCACTGGAAAATGATGTTAAAGTAAGAATTGCAAAA

FIGURE 22

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576
><subunit 1 of 1, 251 aa, 1 stop
><MW: 26935, pI: 7.42, NX(S/T): 2
MAMGVPRVILLCLFGAACLCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSL
DTGYRAPVTLVRKGCGWTGPPAGQTQSNDALPPDYSVVRGCTTDKCNALMTHDALPNLSQA
PDPPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQGSGRMTVGNFSVPVYIRTCHR
PSCTTEGTTSPWTAIDLQGSCCEGYLCNRKSMTQPFTSASATPPRALQVLALLPVLLLVGLSA
```

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 233-251

N-glycosylation sites.

amino acids 120-124, 174-178

N-myristoylation sites.

amino acids 15-21, 84-90

FIGURE 23

CCCCACGCGTCCGGGACAGATGAACCTAAAGAGAAGCTTAGCTGCCAAAGATTGGGAAAGG
GAAAGGACAAAAAAGACCCCTGGGCTACACGGCGTAGGTGCAGGGTTCTACTGCTGTTCT
TTTATGCTGGGAGCTGTGGCTGTAACCAACTAGGAAATAACGTATGCAGCAGCT**ATG**GCTGT
CAGAGAGTTGTGCTTCCAAGACAAAGGCAAGTCCTGTTCTTTCTTTGGGAGTG
CCTTGGCAGGTTCTGGGTTGGACGTTATTGGTACTGAGGAAACAGAGAAGAGATCCTT
GTGGTCAATCTGGCAAAGGATCTGGACTAGCAGAGGGGAGCTGGCTGCAAGGGAAACCAG
GGTGGTTCCGATGATAACAAACAATACCTGCTCCTGGATTCACATACCGGAATTGCTCA
CAAATGAGAAACTGGACCGAGAGAAGCTGTGTCGCCCTAAAGAGGCCCTGTATGCTGTT
CAAATTAAATGGATGATCCCTTCAGATTACCGGGCTGAGCTGAGAGTCAGGGATATAAA
TGATCACGCGCCAGTATTCAGGACAAAGAACAGTCTAAAAATATCAGAAAATACAGCTG
AAGGGACAGCATTAGACTAGAAAGAGCACAGGATCCAGATGGAGGACTTAACGGTATCCAA
AACTACACGATCAGCCCCAACTCTTTCCATATTAAACATTAGTGGCGGTGATGAAGGCAT
GATATATCCAGAGCTAGTGTGGACAAAGCACGGATCGGAGGAGCAGGGAGAGCTCAGCT
TAACCCCTCACAGCGCTGGATGGTGGCTCCATCCAGGTCTGGACCTCTACTGTACGCATC
GTTGTCTGGACGTCAATGACAATGCCAACAGTTGCCAGGCCTGTATGAGACCCAGGC
TCCAGAAAACAGCCCCATTGGGTTCCATTGTTAAGGTATGGCAGAAGATGTAGACTCTG
GAGTCAACGCGGAAGTATCCTATTCACTTTGATGCCCTCAGAAAATATTGAACGACCTT
CAAATCAATCCTTTCTGGGAAATCTTCTCAGAGAATTGCTGATTATGAGTTAGTAAA
TTCTTACAAAATAAATATACAGGCAATGGACGGCTGGAGGCCCTCTGCAAGATGTAGGGTT
TAGTGGAAAGTATTGGACACCAATGACAATCCCCCTGAACACTGATGTTATCATCATTTC
TCTGTTGCTGAGAATTCTCCTGAGACGCCGCTGGCTGTTTAAGATTAATGACAGAGACTC
TGGAGAAAATGGAAAGATGGTTGCTACATTCAAGAGAATCTGCCATTCTACTAAAACCTT
CTGTGGAGAATTTCACATCTTAATTACAGAAGGCGCCTGGACAGAGAGTCAGAGCGAG
TACAACATCACTATCACCCTGACTGACTGGGACACCCAGGCTGAAAACCGAGCACACAT
AACGGTCTGGTCTCGACGTCAATGACAACGCCCGCCTCACCCAAACCTCCTACACCC
TGTTCGTCGGCGAGAACACAGCCCCGCCCTGCACATCGCAGCGTCAGGCCACAGACAGA
GACTCGGGCACCAACGCCAGGTACCTACTCGCTGTCGCCGCCAGAACGCCGACCTGCC
CCTCGCCTCCCTGGTCTCCATCAACCGGACAACGCCACCTGTCGCCCTCAGGTGCTGG
ACTACGAGGCCCTGAGGCTTCGAGTTCCCGTGGGCCACAGACCGCGCTCCCCCGCG
CTGAGCAGAGAGGCCGCTGGTGCCTGCTGGTGTGGACGCCAACGACAACCTGCCCTCGT
GCTGTACCCGCTGCAGAACGGCTCCGCCCTGCACCGAGCTGGTGCCTGGCGGCGAGC
CGGGCTACCTGGTGACCAAGGTGGTGGCGGTGGACGGCGACTCGGGCCAGAACGCCCTGGCTG
TCGTACCGAGCTGCTCAAGGCCACGGAGGCCGGCTGTCGGTGTGGGCCACAATGGGGA
GGTGCACCGCCAGGCTGCTGAGCGAGCGCACGCCAGCAGCACAGGCCGAGGC
TCAAGGACAATGGCGAGCCTCCCGCTCGCTCGGCCACGCCAGCCTGCACTTGCTCCTGGAC
GGCTTCTCCCAGCCCTACCTGCTCTCCCGAGGCCGGCCAGGCCAGGCCGAGGC
CGACTTGCTCACCGTCTACCTGGTGGCGTGGCTGCCCTGGTGTCTCGCTCTCCCTCT
CGGTGCTCTGGTGGCGGTGCCAGGGCTGTCAGGAGGAGCAGGGCGGCCCTGGTGGCG
TGCTCGGTGCCCGAGGGCTTCCAGGGCATCTGGTGGACGTGAGGGCGCTGAGACCCCT
GTCCCAGAGCTACCACTGAGGTGTCTGACGGGAGGCCGCCAGTGAAGTTCAAGT
TCTGAAACCAAGTTATTCGGATATTCAAGGCACAGGCCCTGGAGGAAGGGTGAAGAAAAT
TCCACCTTCGAAATAGCTTGGATTAATATTCAAG**TAA**AGTCTGTTTAGTTCATATAAC
TTTGGTGTGTTACATAGCCATGTTCTATTAGTTACTTTAAATCTCAAATTAAAGTTAT
TATGCAACTCAAGCATTATTTCAAGTAGTATACCCCTGTTGTTACAATGTTCATCAT
TTTTTGCTTAATAACAACGGTTAATTAAATGAGTATTGTTCTAAATGATAGTGT
AAGGTTTAATTCTTCAACTGCCAAGGAATTAAATTACTATTATATCTCATTACAGAAAT
CTGAGGTTTGATTCACTTCAAGAGCTGCTCATGATTCTAATCACTTCTGTCTATAGT
TACCTGCTCTATTAAGAAGGCATATCTACATTCCAAACTCATCTAACATTCTATATATT
CGTGGTGGAAAACCATGTCATTATTCTACATCATGTATTAAAAAGAAATATTCTCTAC
TACTATGCTCATGACAAAATGAAACAAAGCATATTGTGAGCAATACTGAACATCAATAAC
CCTTAGTTATATACTTATTATTTATCTTAAGCATGCTACTTTACTTGGCCAATATT
CTTATGTTAACTTTGCTGATGTATAAAACAGACTATGCCCTATAATTGAAATAAAATTATA
ATCTGCCCTGAAATGAATAAAACATTGAAATGTGAAAAAAAAAAAAAA

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA87976

><subunit 1 of 1, 800 aa, 1 stop

><MW: 87621, pI: 4.77, NX(S/T): 7

MAVRELCFPRQRQVLFLFWGVSLAGSGFGRYSVTEETEKGSFVVNLAKDLGLAEGELAAR
GTRVVSDDNKQYLLLDSHTGNLLTNEKDREKLCPKEPCMLYFQILMDDPFQIYRAELRVR
DINDHAPVFQDKETVLKISENTAEGTAFRLERAQDPDGGLNGIQNYTISPNSFFHINISGGD
EGMIYPELVLDKALDREEQGELSLLTALDGGSPSRSGTSTVRIIVLDVNNDNAPQFAQALYE
TQAPENSPIGFLIVKVWAEDVDGVNAEVSYSSFDASENIRTTFQINPFSGEIFLRELLDYE
LVNSYKINIQAMDGGGLSARCRVLVEVLDTNPPPELIVSSFSNSVAENSPETPLAVFKIND
RDSGENGMVCYIQENLPFLLKPSVENFYILITEGALDREIRAEYNITITVTDLGTPLRKTE
HNITVLVSDVNDNAPAFQTSYTLFVRENNSPALHIGSVSATDRDGTNAQVTYSLLPPQDP
HLPLASLVSINADNGHLFALRSLDYEALQAFEFRVGATDRGSPALSREALVRVLVLDANDNS
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATEPGLFGVWAH
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHLLVDGFSQPYLPLPEAAPAQAO
AEADLLTVYLVVALASVSSLFLSVILLFVAVRLCRRSRAASVGRCSVPEGFPGLVVDVRGA
ETLSQSYQYEVCLTGGPGTSEFKFLKPVISDIQAQGPGRKGEENSTFRNSFGFNIQ

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 687-711

N-glycosylation sites.

amino acids 169-173, 181-185, 418-422, 436-440, 567-571, 788-792

Glycosaminoglycan attachment site.

amino acids 28-32

Tyrosine kinase phosphorylation sites.

amino acids 394-402, 578-585

N-myristoylation sites.

amino acids 22-28, 27-33, 53-59, 82-88, 162-168, 184-190,
217-223, 324-330, 325-331, 471-477, 568-574, 759-765

Amidation site.

amino acids 781-785

Aminoacyl-transfer RNA synthetases class-II signature 1.

amino acids 117-138

Cadherins extracellular repeated domain signature.

amino acids 121-132, 230-241, 335-346, 439-450, 549-560

FIGURE 25

GAATGAATACTCCGAAGCCGTTTGTCTCCAGATGTGAATAGCTCCACTATACCAGCCTC
GTCTTCCTTCCGGGGACAACGTGGGTCAAGGCACAGAGAGATATTAATGTCACCCTTTG
GGGCTTCATGGACTCCCTGCCACATTGGAGGTTGGAAAGTTGCTAGAGGCTTC
AGAACTCCAGCCTA**ATG**GATCCAAACTCGGGAGAATGGCTGCGCCCTGCTGGCTGTGCTG
CTGCTGCTGCTGGAGCGCGCATGTTCTCCTCACCCCTCCCCGCCCGCGCTGTTAGAGAA
AGTCTTCAGTACATTGACCTCCATCAGGATGAATTGTCAGACGCTGAAGGAGTGGTGG
CCATCGAGAGCGACTCTGTCCAGCCTGCGCTCGCTCAGACAAGAGCTTCAGAATGATG
GCCGTGGCTGCGGACACGCTGCAGGCCTGGGGCCCGTGTGGCCTCGGTGGACATGGTCC
TCAGCAGCTGCCGATGGTCAGAGTCTCCAATACCTCCGTATCCTGGCGAAGTGGG
GCGATCCCACGAAAGGCACCGTGTGCTCTACGGCCACTGGACGTGCGAGCCTGCTGACCG
GGCGATGGGTGGCTACGGACCCCTATGTGCTGACGGAGGTAGACGGAAACTTATGGACG
AGGAGCGACCGACAACAAAGGCCCTGTCTGGCTGGATCAATGCTGTGAGCGCCTCAGAG
CCCTGGAGCAAGATCTCCTGTGAATATCAAATTCATATTGAGGGATGGAAGAGGCTGGC
TCTGTTGCCCTGGAGGAACTTGGAAAAAGAAAAGGACCGATTCTCTGGTGTGGACTA
CATTGTAATTTCAGATAACCTGTGGATCAGCAAAGGAAGGCCAGCAATCACTATGGAACCC
GGGGAACAGCTACTTCATGGTGAGGTGAAATGCAGAGACCAGGATTTCACTCAGGAACC
TTTGGTGGCATCCTCATGAACCAATGGCTGATCTGGTGCTCTCTCGTAGCCTGGTAGA
CTCGTCTGGTCATATCCTGGCCCTGGAATCTATGATGAAGTGGTCTCTACAGAACAGGG
AAATAAATACATACAAAGCCATCCATCTAGACCTAGAAGAACACCGGAATAGCAGCCGGGTT
GAGAAATTCTGTTGATACTAAGGAGGAGATTCTAATGACACCTCTGGAGGTACCCATCTCT
TTCTATTGACTGGATCGAGGGCGCGTTGATGAGCCTGGAACCTAAACAGTCATACCTGGCC
GAGTTATAGGAAATTTCATCCGTCTAGTCCCTCACATGAATGTCCTGGTGGAAAAAA
CAGGTGACACGACATCTGAAGATGTTCTCAAAGAAATAGTCCAACAAAGATGGTTGT
TTCCATGACTCTAGGACTACACCCGTGATTGCAAATATTGATGACACCCAGTATCTCGCAG
CAAAAGAGCGATCAGAACAGTGTGGAACAGAACAGAGATATGATCCGGATGGATCCACC
ATTCCAATTGCCAAATGTTCCAGGAGATGTCACAGAGCGTGGTCTAATTCCGCTGGG
AGCTGTTGATGATGGAGAACATTGCGAGAATGAGAAATCAACAGGTGGAACATAGAGG
GAACCAAATTATTGCTGCCTTTCTTAGAGATGGCCAGCTCCATTAAATGTCCTG
TCTAGTCTGATCTGATCCACTGACAGATTCACCTCCCCACATCCCTAGACAGGGATGGAAT
GTAAATATCCAGAGAACATTGGTCTAGTATAGTACATTTCCTCCATTAAATGTCCTG
GGATATCTGGATCAGTAATAAAATATTCAAAGGCACAGATGTTGAAATGGTTAAGGTCC
CCCACTGCACACCTCCTCAAGTCAGTCTGCTGCAGCAACTTGATTTCCCAAGTCCTGT
GCAATAGCCCCAGGGATTGGATTCCTCCAACCTTTAGCATATCTCAACCTGCAATTGA
TTGGCATAATCACTCCGGTTGCTTCTAGGTCTCAAGTGCTCGTACACATAATCATTCC
ATCCAATGATCGCCTTGCTTACCACTCTTCTTTATCTTATTAAATAAAAATGTTGGTC
TCCACCACTGNCTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAA

FIGURE 26

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92234
><subunit 1 of 1, 507 aa, 1 stop
><MW: 56692, pI: 5.22, NX(S/T): 3
MDPKLGRMAASLLAVLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESD
SVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTK
GTVCFYGHLDVQPADRGDGWLTDYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQD
LPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSY
FMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTY
KAIHLDLEEYRNSSRVEKFLFDTKEEILMHWRYPQLSIHGIEGAFDEPGTKTVIPGRVIGK
FSIRLVPHMNNSAVEKVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAI
RTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF
AAFFLEMAQLH
```

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

273-292

N-glycosylation sites.

amino acids 322-326, 382-386, 402-406

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 400-404

N-myristoylation sites.

amino acids 89-95, 119-125, 162-168, 197-203, 242-248, 263-269,
351-357

Cell attachment sequence.

amino acids 140-143

ArgE / dapE / ACY1 / CPG:

amino acids 156-167

FIGURE 27

CTCGGCTGGATTAAAGGTTGCCGCTAGCCGCCTGGGAATTAAAGGGACCCACACTACCTTCC
CGAAGTTGAAGGCAAGCGGTGATTGTTGTAGACGGCGCTTGTCATGGGACCTGTGCGGTT
GGGAATATTGCTTTCTTTGGCCGTGCACGAGGCTGGGCTGGGATGTTGAAGGAGG
AGGACGATGACACAGAACGCTGCCAGCAAATGCGAAGTGTGTAAGCTGCTGAGCACAGAG
CTACAGGCGGAACGTGAGTCGACCGGTGATCTCGAGAGGTGCTGGAGCTGGGCAGGTGCT
GGATAACAGGCAAGAGGAAGAGACACGTGCCTACAGCGTTCAGAGACAAGGCTGGAAGAGG
CCTTAGAGAATTATGTGAGCGGATCCTGGACTATAGTGTTCACGCTGAGCGCAAGGGCTCA
CTGAGATATGCCAAGGGTCAGAGTCAGACCATGGCAACACTGAAAGGCCTAGTGCAGAAGGG
GGTGAAGGTGGATCTGGGATCCCTCTGGAGCTTGGGATGAGCCCAGCGTGGAGGTACAT
ACCTCAAGAACAGCAGTGTGAGACCATGTTGGAGGGAGTTGAAGACATTGTGGGAGACTGGTAC
TTCCACCATCAGGAGCAGCCCCAACAAAATTTCTCTGTGAAGGTCATGTGCTCCAGCTGC
TGAAACTGCATGTCTACAGGAAACTTGGACTGGAAAGGAGATCACAGATGGGAAGAGAAAA
CAGAAGGGGAGGAAGAGCAGGAGGAGGAGGAAGAGGAGGAAGAGGAAGGGGGAGACAAG
ATGACCAAGACAGGAAGCCACCCAAACTGACCGAGAAGATCTTTGACCCTGCCTTGAG
CCCCCAGGAGGGAAAGGGATCATGGAGAGCCCTCTAAAGCCTGCACTCTCCCTGCTCCACAG
CTTCAGGGTGTGTTATGAGTGACTCCACCCAAAGCTTGTAGCTGTTCTCTCCATCTAAC
TCAGGCAAGATCCTGGTAAACAGCATGACATGGCTCTGGGGTGGAGGGTGGGGGTGGAGG
TCCTGCTCCTAGAGATGAACCTATCCAGCCCCTTAATTGGCAGGTGTATGTGCTGACAGTA
CTGAAAGCTTCCTTTAACTGATCCCACCCCCACCCAAAAGTCAGCAGTGGCACTGGAGC
TGTGGGCTTGGGAAGTCACTTAGCTCCTTAAGGTCTGTTTAGACCCTCAAGGAAGA
GGCCAGAACGGACATTCTCTGCGATCTATACATTGCCTGTATCCAGGAGGCTACACACCA
GCAAACCGTGAAGGAGAATGGGACACTGGGTATGGCCTGGAGTTGCTGATAATTAGGTGG
GATAGATACTTGGTCACTTAAGCTCAATGTAACCCAGAGCCCACCATATAAGTTTATAGGT
GCTCAACTTCTATATCGCTATTAAACTTTTCTTTCTA

FIGURE 28

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92256
><subunit 1 of 1, 248 aa, 1 stop
><MW: 28310, pI: 4.63, NX(S/T): 0
MPGPVRLGILLFLFLAVHEAWAGMLKEEDDDTERLPSKCEVCKLLSTELQAEALSRTGRSREVL
ELGQVLDTGKRKRHVPYSVSETRLEEALENLCERILDYSVHAERKGSLRYAKGQSQTMATLK
GLVQKGVVKVDLGIPPLELWDEPSVEVTYLKKQCETMLEEFEDIVGDWYFHHQEQPLQNFLCEG
HVLPAAETACLQETWTGKEITDGEETEGEEEEEEGGDKMTKTGSHPKLDREDL
```

Important features of the protein:

Signal peptide:

amino acids 1-21

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 106-110

N-myristoylation site.

amino acids 115-121

Amidation site.

amino acids 70-74

FIGURE 29

AAGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCCTT
CTCCCTGTGCTTAACCAGAGGTGCCCAATGGGTTGGACAATGAGGCTGGTACAGCAGCACTG
TTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCCTGTGCCCATGA
GCCCTCTGGACGAGGACACCCTTTGCCAGGGCCTTGAAGTTTCTACCCAGAGTTGG
GGAACATTGGCTGCAAGGTTGTTCTGATTGTAACAACATACAGACAGAACAGATCACCTCCTGG
ATGGAGCCGATAGTCAAGTTCCGGGGCGTGGACGGCGAACCTATATCCTGGTATGGT
GGATCCAGATGCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAA
CAGATATCAAGGGCGCCGACCTGAAGAAAGGAAGATT CAGGGCCAGGAGTTATCAGCCTAC
CAGGCTCCCTCCCCACCGGACACAGTGGCTTCCATCGCTACCAGTTCTGTCTATCTTCA
GGAAGGAAAAGTCATCTCTCCTCCAAGGAAAACAAAACGAGCTCTGGAAAATGG
ACAGATTCTGAACCGCTTCCACCTGGCGAACCTGAAGCAAGCAGCAGTTATGACCCAG
AACTACCAGGACTCACCAACCCCTCCAGGCTCCCAGAGGAAGGGCCAGCGAGCCAAGCACAA
AACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGTTGCCATCCGGCATGTGCCACAC
TGCTCACCAACCGACGATGTGGGTATGGAACCCCTCTGGATACAGAACCCCTTCTTCAA
ATTAAAAAAAAAAATCATAAA

FIGURE 30

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92274
><subunit 1 of 1, 223 aa, 1 stop
><MW: 25402, pI: 8.14, NX(S/T): 1
MGWTMRLVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPELGNIGCKVVP
DCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSRAEPRQRFWRWLVTEDIKGADLK
KGKIQGQELSAQAPSPPAHSGFHRYQFFVYLQEGKVISLLPKENKTRGSWKMDRFLNRFHL
GEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQR
```

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 169-173

Tyrosine kinase phosphorylation site.

amino acids 59-68

N-myristoylation sites.

amino acids 54-60, 83-89, 130-136

Phosphatidylethanolamine signature.

amino acids 113-157

FIGURE 31

GTCGACCCACCGTCCGAAGCTGCTGGAGCCACGATTCACTCCCCTGGACTGTAGATAAAGA
CCCTTTCTGCCAGGTGCTGAGACAACCACACTATGAGAGGCACTCCAGGAGACGCTGATGG
TGGAGGAAGGGCCGTCTATCAATCAATCACTGTTGCTTATCACATGCAAGTATCCAGAGG
CTCTTGAGCAAGGCAGAGGGATCCCATTATTGGGAATCCAGAAATCCAGAAATGTGTTG
TATTGTGAGAAGGTTGGAGAACAGCCCACATTGCAGCTAAAAGAGCAGAAGATCATGGATCT
GTATGGCCAACCCGAGCCGTGAAACCCCTCCTTCTACCGTGCCAAGACTGGTAGGACCT
CCACCCCTGAGTCTGTGGCCTCCGGACTGGTCATTGCCTCCTCCAAGAGAGACCAGCCC
ATCATTCTGACTTCAGAACTGGGAAGTCATACAACACTGCCTTGAATTAAATATAATGA
CTGAACTCAGCCTAGAGGTGGCAGCTGGTCTTGTCTAAAGTTCTGGTCCCAATGTGT
TTTCGTCTACATTTCTTAGTGTCTTTCACGCTGGTGTGAGACAGGGAGCAAGGCTGCTG
TTATCATCTCATTATATAATGAAGAAGCAATTACTCATAGCAACTGAAGAACAGGATG
TGGCCTCAGAAGCAGGAGAGCTGGGTGTTAAGGCTGTCCTCTCAAGCTGGTGTGCTG
GCCACAAGGCATCTGCATGAGTGACTTAAGACTCAAAGACCAAAACTGAGCTTCTCTA
GGGGTGGGTATGAAGATGCTTCAGAGCTCATGCGCTTACCCACGATGGCATGACTAGCACA
GAGCTGATCTCTGTTCTGTTGCTTATTCCCTCTGGGATGATATCATCCAGTCTTAT
ATGTTGCCAATATAACCTCATTGTGTAAATAGAACCTCTTAGCATTAAAGACCTTGTAAACA
AAAATAATTCTTGGGGTGGGTATGAAGATGCTTCAGAGCTCATGCGCTTACCCACGATGGC
ATGACTAGCACAGAGCTGATCTGTTCTGTTGCTTATTCCCTCTGGGATGATATCA
TCCAGTCTTATATGTTGCCAATATAACCTCATTGTGTAAATAGAACCTCTTAGCATTAAAG
ACCTTGTAAACAAAATAATTCTTGTGTTAAGTTAAATCATTGTCCTAATTGTAAATGTG
TAATCTTAAAGTTAAATAAACTTGTGTTATTATATAATAAAAGCTAAAACGTGATATAAA
ATAAAGAAAGAGTAAACTG

FIGURE 32

MRGTPGDADGGGRAVYQSITVAVITCKYPEALEQGRGDPYLGQNPEMCLYCEKVGEQPTL
QLKEQKIMDLYGQPEPVKPFLFYRAKTGRTSTLESVAFPDWFIASSKRDQPIILTSELGKSY
NTAFELNIND

Signal sequence:

amino acids 1-17

N-myristoylation site.

amino acids 10-16

Cell attachment sequence.

amino acids 36-39

FIGURE 33

GCGAGGCTGCACCAGGCCCTGGCACC**ATG**AGGACGCCCTGGCCTCTGCCCGTGTGCTGCTGCTG
CTCCTGGCGGGAGCCCCGCCGCGCGGCCACTCCCCGACCTGCTACTCCCGCATGCGGGC
CCTGAGCCAGGAGATCACCCGCGACTTCAACCTCCTGCAGGTCTCGAGGCCCTGGAGGCCAT
GTGTGAGATACTGCCAGGCTGTACCTGGACATACACAATTACTGTGTGCTGGACAAGCTG
CGGGACTTGTGGCCTGCCCGTGTGGAAAGTGGCCCAGGTAGATTCTGAAGGACAA
AGCACGGAAGCTGTACACCATCATGAACTCGTTCTGCAGGAGAGATTGGTATTCTGTGTTGG
ATGACTGCAATGCCTTGAATACCAATCCCAGTGACTACGGTCCTGCCAGATCGTCAGCGC
TAAGGGAACGTGAGACCAGAGAAAGAACCCAAGAGAACTAAAGTTATGTCAGCTACCCAGACT
TAATGGGCCAGAGCCATGACCCCTCACAGGTCTTGTGTTAGTTGTATCTGAAACTGTTATGTA
TCTCTCTACCTCTGGAAAACAGGGCTGGTATTCTCACCCAGGAACCTCCTTGAGCATAGA
GTTAGCAACCATGCTCTCATTCCCTTGACTCATGTCCTGCCAGGATGGTAGATACACAGC
ATGTTGATTGGTCACTAAAAAGAAGAAAAGGACTAACAGCTTCACTTTATGAACAACTA
TTTGAGAACATGCACAATAGTATGTTTATTACTGGTTAATGGAGTAATGGTACTTTA
TTCTTCTTGATAGAACCTGCTTACATTAAACCAAGCTCTATTATGCCCTTTCTAACAC
AGACTTTCTTCACTGCTTCATTAAAAAGAAATTAAATGCTCTTAAGATATATATTTACG
TAGTGCTGACAGGACCCACTTTCAATTGAAAGGTGATGAAAATCAAATAAGAATCTCTC
ACATGGA

FIGURE 34

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA93011
><subunit 1 of 1, 136 aa, 1 stop
><MW: 15577, pI: 8.88, NX(S/T): 0
MRTPGPLPVLLLLLAGAPAARPTPPTCYSRMALSQEITRDFNLLQVSEPSEPCVRYLPRLY
LDIHNVCVLDKLRDFVASPPCWKVAQVDSLKDARKLYTIMNSFCRRDLVFLLDDCNALEYP
IPVTTVLPDRQR
```

Important features of the protein:

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site.

amino acids 60-69

N-myristoylation site.

amino acids 16-22

FIGURE 35

GTCTCCGCGTCACAGGAACCTCAGCACCCACAGGGCGGACAGCGCTCCCTCTACCTGGAGA
CTTGACTCCCGCGCCCCAACCTGCTTATCCCTTGACCGTCGAGTGTAGAGATCCTGCA
GCCGCCAGTCCCAGCCCCCTCTCCGCCCCACACCCACCCCTCCTGGCTCTCCTGTTTAC
TCCTCCTTTCATTATAACAAAAGCTACAGCTCCAGGAGCCCAGCGCCGGCTGTGACCCA
AGCCGAGCGTGGAAAGAATGGGGTCCTCGGGACCAGGCACTTGGATTCTGGTGTAGTGCTCC
CGATTCAAGCTTCCCCAACCTGGAGGAAGCCAAGACAAATCTACATAATAGAGAATTA
AGTGCAGAAAGACCTTGAATGAACAGATTGCTGAAGCAGAAGAAGACAAGATTAAAAAAAAC
ATATCCTCCAGAAAACAAGCCAGGTCAAGAGCAACTATTCTTGATAACTTGAACCTGC
TAAAGGCAATAACAGAAAAGGAAAAATTGAGAAAGAAAGACAATCTATAAGAAGCTCCCCA
CTTGATAATAAGTTGAATGTGGAAGATGTTGATTCAACCAAGAACATCGAAAACGTGATG
TTATGACTCTACTAAGAGTGGAATTGGATCATAAATTCAAGATGATCCAGATGGTCTTCATC
AACTAGACGGGACTCCTTAACCGCTGAAGACATTGTCATAAAATCGCTGCCAGGATTAT
GAAGAAAATGACAGAGCCGTGTTGACAAGATTGTTCTAAACTACTTAATCTCGGCCATT
CACAGAAAGCCAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTACAAAATTATCT
CAAAGGAAGCCAACAATTATGAGGAGGATCCAAATAAGCCCACAAGCTGGACTGAGAACATCAG
GCTGGAAAATACCAAGAGAAAGTGAATCCAATGGCAGCAATTCAAGATGGTCTTGCTAAGGG
AGAAAACGATGAAACAGTATCTAACACATTAACCTTGACAATGGCTGGAAAGGAGAACTA
AAACCTACAGTGAAGACAACATTGAGGAACCTCAATATTCCAAATTCTATGCGCTACTG
AAAAGTATTGATTGAGGAAAGCAGGAAAGAGAAAGAACACTGATTACTATCATGAAAAC
ACTGATTGACTTGTGAAGATGATGGTGAATATGGAACAATATCTCCAGAAGAAGGTGTT
CCTACCTGAAAACCTGGATGAAATGATTGCTCTCAGACCAAAACAAGCTAGAAAAAAAT
GCTACTGACAATATAAGCAAGCTTCCCAGCACCACAGAGAAGAGTCATGAAGAAACAGA
CAGTACCAAGGAAGAACGCTAACAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCCACAA
AAGATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAACAGAACGCTAT
TTGGAAGCCATCAGAAAAAATTGAATGGTGAAGAACATGACAAAAGGAAATAAAGA
AGATTATGACCTTCAAAGATGAGAGACTTCATCAATAAACAGCTGATGCTTATGTGGAGA
AAGGCATCCTGACAAGGAAGAACGCGAGGCCATCAAGCGCATTATAGCAGCCTGTAAA
TGGCAAAAGATCCAGGAGTCTTCAACTGTTCAGAAAACATAATAGCTAAAACACTTC
TAATTCTGTGATTAAAATTGGTGAAGGTTATTAGAAAGTGCTGAATTACAGTAGT
TAACCTTTACAAGTGGTAAAACATACTGTTCTCCGTAAAACATCTGAAAGTAAAGT
TGTATGTAAGCTGAAAAAAAAAAAAAA

FIGURE 36

MGFLGTGTWILVLVLPIQAFPKPGSQDKSLHNRELSAERPLNEQIAEAEEEDKIKKTYPPEN
KPGQSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTK
SGLDHKFQDDPDGLHQLDGTPHTAEDIVHKIAARIYEENDRAVFDFKIVSKLLNLGLITESQA
HTLEDEVAEVVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTMMAAIQDGLAKGENDET
VSNTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFV
KMMVKYGTISPEEGVSYLENLDEMIALQTKNKNATDNISKLFPAPSEKSHEETDSTKEE
AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKGKNDYDLS
KMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL

N-glycosylation sites:

amino acids 68-71, 346-349, 350-353

Casein kinase II phosphorylation site:

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-
341, 369-372, 382-385, 386-389, 387-390

N-myristoylation sites:

amino acids 143-148, 239-244

FIGURE 38

MALPPGPAALRHTLLLLPALLSSGWGELEPQIDGQTWAERALRENERHAFTCRVAGGGPGTPRLAWYLDGQLQEASTSRLLSVGGEAFSGGTSTFTVTAHRAQHELNCSLQDPRSGRSANASVILNVQFKPEIAQVGAKYQEAQGPGLLVVLFALVRANPPANVTWIDQDGPVTVNNTSDFLVLDQNYPWLTNHTVQLQLRSLAHNLSVVATNDGVTSASLPAPGPSRHPSLISSDSNNLKLNNVRLPRENMSLPSNLQLNDLTPDSRAVKPADRQMAQNNSRPELLDPEPGGLTSQGFIRLPVLGYIYRVSSVSSDEIWL

N-glycosylation sites:

amino acids 106-110, 119-123, 162-166, 175-179, 192-196, 205-209, 251-255, 280-284

Glycosaminoglycan attachment site:

amino acids 23-27

Casein kinase II phosphorylation sites:

amino acids 36-40, 108-112, 164-168, 282-286, 316-320

N-myristoylation sites:

amino acids 34-40, 89-95, 215-221, 292-298, 293-299

FIGURE 39

CGGGGACGGAAGCGCCCCCTGGGCCCGAGGGGCTGGAGCCGGGCCGGCG**ATGT**GGAGCGC
GGGCCGCGCGGGCTGCCTGGCCGGTGCCTGGGGCTGCTGCTGGCGCTGTTAGTGCCGG
GCGGTGGTGCCGCCAAGACCGGTGCAGGACTCGTACCTGCAGCACATCAAATACGGATCCGGCAGCGGCCA
AATACGCACCACCGCGTGCAGGCTGCACCGACATCAAATACGGATCCGGCAGCGGCCA
GCAATCGGTGACCGGGTAGAGGGCGTCGGACGACGCCAATAGCTACTGGCGGATCCGGCG
GCTCGGAGGGCGGGTGCCTGGCGCGGGTCCCCGGTGCCTGCAGGCGAGGCGTCAAC
CATGTGCTTACGGCAAGAACCTGCACACGCACTTCCGTGCCGCTGTCCAACAACCA
GGAGGTGAGTGCCTTGGGAAGACGGCGAGGGGACGACCTGGACCTATGGACAGTGC
GCTCTGGACAGCACTGGAGCGTGAGGCTGCTGTGCCTCCAGCATGTGGCACCTCTGT
TTCCTGTCAGTCACGGTGAGCAGTATGGAAGCCCCATCCGTGGCAGCATGAGGTCCACGG
CATGCCCAAGTGCACACGACAATACGTGGAAGGCCATGGAAGGCATCTCATCAAGCCTA
GTGTGGAGCCCTCTGCAGGTACGATGAACCT**TGA**GTGTGGATGGATGGGTGGATGGAGG
GTGGCAGGTGGGGCGTCTGCAGGCCACTCTGGCAGAGACTTGGTTGTAGGGTCCTC
AAGTGCCTTGTGATTAAAGAATGTTGGTCTATGAAA

FIGURE 40

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96857
><subunit 1 of 1, 221 aa, 1 stop
><MW: 23598, pI: 6.96, NX(S/T): 0
MWSAGRGGAAWPVLLGLLLALLVPGGGAAKTGAELVTCGSVLKLLNTHHRVRLHSHDIKYGS
GSGQQSVTGVVEASDDANSYWRIRGGSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFPSPL
SNNQEVSAGFEGEDGEGLDLWTVRCSGQHWEREAAVRFQHVGTSVFLSVTGEQYGSPIRGQH
EVHGMPSANTHNTWKAMEGIFIKPSVEPSAGHDEL
```

Important features of the protein:

Signal peptide:

amino acids 1-28

Glycosaminoglycan attachment site.

amino acids 62-66

N-myristoylation sites.

amino acids 16-22, 25-31, 27-33, 61-67, 71-77, 86-92, 87-93,
91-97, 190-196

Endoplasmic reticulum targeting sequence.

amino acids 218-223

FIGURE 41

GTTGCTATGTTGCCAGGCTGGTCTTGAAGTGCCTGACCTCCTAAAGTGTGGAACCACAG
ACGTGAGCCACTCCACCCAGCCTAAAACATCCTCTTGGATGAGATAACACTTTAAC
AAGAGAACAGGACTCTATATAAATCGCTGTGGCTCACCACTCTAAGGAGGAGCACTGACT
GAAGACAGAAAAATTGATGAAGAAGACATGGCATTATGCCTACAAACTACACA
GTGCTTGGAATTCAAAGTACTCAGTGGAGAGAGGTGTTCAGGAGCCGTAGAGCCAGAT
CGTCATC**ATG**TCTGCATTGTGGCTGCTGGCTCCTGCCCTGATGGACTTGTCTGAAA
GCAGCAACTGGGATGCTATGAAACATCCAAAGCCTGGACACCCCTGGAGCATCTGTGG
ATTGGAAGACGTACGGCCTGAAACTACTGTGGAGTTCGTCTGAAAGGCTGGCTGAAAT
AGACATGCCATACCTCCTGAAATATCAACCCATGATGCAAACCATGGCAAAGTACTGCA
TGGATCCTGCCGTGATCGCTGGTGTCTGTCCAGGAAGTCTCCGGTACAAAATTCTGGTC
AACATGGCGATAGGACTAGCATGGTGCAGGACCCCTGGCTCTCAAGCTCCACATCCTGGAT
TAGTGAGTCTCAGGTTCCCAGACAACACTGAAGTTCTGACTACTAGAATCAAAGAAATCCAGA
GGAGGTTCCAACCTGGACCCCTGACCAGTACCTGAGAGGTGGACTCTGTGCCTACAGTGG
GGTCTGGCTATGTCCGAAGCAGCCAGGACCTGAGCTGTGACTCTGCAATGATGTCCCTG
ACGAGCCAAGTACCTCAAGAGACATGGCTTC**TAA**CATCTCAGATGAAACCCAAGACCATGAT
CACATATGCAGCCTCAAATGTACACAGATAAAACTAGCCAAGGGCACCTGTAACGGAAAT
CTGAGTTGACCTAAAGTCATTAAATAACATGAATCCCATTAAAAAAAAAAAAAA

FIGURE 42

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96867
.><subunit 1 of 1, 194 aa, 1 stop
><MW: 21431, pI: 8.57, NX(S/T): 0
MSALWLLLGLLALMDLSESSNWGCYGNIQSLDTPGASCIGRRHGLNYCGVRASERLAEIDM
PYLLKYQPMMQTIGQKYCMDPAVIAGVLSRKSPGDKILVNMGDRTSMVQDPGSQAPTSWISE
SQVSQTTEVLTTRIKEIQRRFPTWTPDQYLRGGLCAYSGGAGYVRSSQDLSCDFCNDVLARA
KYLKRHGF
```

Important features of the protein:

Signal peptide:

amino acids 1-19

N-myristoylation sites.

amino acids 23-29, 26-32, 35-41, 45-51, 50-56, 76-82, 156-162

Amidation site.

amino acids 40-44

FIGURE 43

TTGAAAATCTACTCTATCAGCTGCTGGTTGCCACCATTCTCAGGACCCTCGCCATGAAAG
CCCTTATGCTGCTCACCCCTGCTGTTCTGCTCTGCTGGGTCTCAGCTGACATTGCTGTCAC
TCCTGCTACAAGGTCCCTGTGCTGGCAGGGCAGTCCTGCCGCCTGGAGGCCAGG
ACAGCAATGCCTGACAACACATGCATACTGGTAAGATGTGGGTTTCTCCAATCTGCGCT
GTGGCACACCAGAAGAGGCCCTGTCAGGAGGCCTAACCAAACCAACCGCAAGCTGGGTCTG
ACATATAAACACCACCTGCTGCAACAAGGACAAC TGCAACAGCGCAGGACCCC GGCCC ACTCC
AGCCCTGGCCTTGTCTCCTTACCTCCTGGCTGGCCTCTGGCTGCTGCACTGAG
ACTCATTCCATTGGCTGCCCTCCTCCCACCTGCCTGGCCTGAGCCTCTCCCTGTGTCT
CTGTATCCCCCTGGCTTACAGAATCGTCTCTCCCTAGCTCCATTCTTAATTAAACACTG
TTCCGAGTGGTCTCCTCATCCATCCTCCCACCTCACACCCTTCACTCTCCTTTCTGGT
CCCTTCCCACCCCTCCAGGACCTCCATTGGCTCTAGAAGGGCTCCCCACTTGCTTCCT
ATACTCTGCTGTCCCCTACTTGAGGAGGGATTGGGATCTGGCCTGAAATGGGCTCTGTG
TTGTCCCCAGTGAAGGCTCCCACAAGGACCTGATGACCTCACTGTACAGAGCTGACTCCCCA
AACCCAGGCTCCCATATGTACCCATCCCCACTCACCTCTTCCATTGAGTAATAAA
TGTCTGAGTCTGGAAAAAAAAAAAAAAA

FIGURE 44

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96878
><subunit 1 of 1, 125 aa, 1 stop
><MW: 13821, pI: 8.60, NX(S/T): 2
MKALMLLTLSVLLCWVSADIRCHSCYKPVLCVDRQSCRLEPGQQCLTTHAYLGKMWVFSN
LRCGTPEEPCQEAFNQTNRKLGLTYNTTCCNKDNCNSAGPRPTPALGLVFLTSAGLGLWLLH
```

Important features of the protein:

Signal peptide:

amino acids 1-18

N-glycosylation sites.

amino acids 77-81, 88-92

N-myristoylation site.

amino acids 84-90

Ly-6 / u-PAR domain protein signature.

amino acids 85-98

FIGURE 45

ACGGGCCGAGCGCAGT GACGTAGGGTTGGCGCACGGATCCGTTGC GGCTGCAGCTCTGCA
GTCGGGCCGTTCTCGCCGCCAGGGTAGCGGTAGCTGCGCAGCGTCGCCGCGCT
ACCGCACCCAGGTCGGCCCCTAGCGTCTGGCAGCCGGCCATCTCATCGAGCGCC**AT**
GGCGCAGCCTGCGGGCCGGGAGCGGGCGGGTACTGCTGCTCCTGGCTGCATTGTTTC
TGCTGACC CGGGCCCTGCCCTGGCTGGAACGACCCCTGACAGAATGTTGCTGC GGATGTA
AAAGCTCTTACCCCTCCACTATGACCGCTATA CCACCTCCGCAGGCTGGATCCC ATCCCACA
GTTGAAATGTGTTGGAGGCACAGCTGGTTGTGATTCTTACCCCCAAAAGTCATACAGTGTG
AGAACAAAGGCTGGATGGGTATGATGTACAGTGGGAATGTAAGACGGACTTAGATATTGCA
TACAAATTGGAAAAACTGTGGTGAGCTGTGAAGGCTATGAGTCCTCTGAAGACCAGTATGT
ACTAAGAGGTTCTTGTGGCTTGGAGTATAATTAGATTATACAGAACTTGGCCTGCAGAAC
TGAAGGAGTCTGAAAGCAGCACGGCTTGCCTCTTCTGATTATTATAAGTGGTCC
TCGGCGGATT CCTGTAACATGAGTGGATTGATTACCATCGTGGTACTCCTTGGATCGCCTT
TGTAGTCTATAAGCTGTTCTGAGTGACGGCAGTATTCTCCTCCACCGTACTCTGAGTATC
CTCCATTCCCACCGTTACCAGAGATTCCA ACTCAGCAGGACCTCCTCCCCCAGGCTTT
AAGTCTGAGTTCACAGGACCACAGAATACTGCCATGGTCAACTCTGGTTTGGCAGTGC
TTTACAGGACAACAAGGATATGAAAATT CAGGACCAGGGTTCTGGACAGGCTTGGAACTG
GTGGAATACTAGGATATTGTTGGCAGCAATAGAGCGCAACACCCTCTCAGACTCGTGG
TACTACCCGTCCTATCCTCCCTACCCCTGGCACGTGAATAGGGCTTACTCACCCCTCA
TGGAGGCTCGGGCAGCTATTGGTATGTTCAAACCTCAGACACGAAAACCAGAACTGCATCAG
GATATGGTGGTACCAGGAGACG**A**TAAAGTAGAAAGTGGAGTCAAACACTGGATGCAGAAAT
TTGGATTTTCACTTTCTCTTACAAAAAAAGTACTACCTGTTAACAAATTGGAAAAG
GGGATATTCAAAGTTCTGTGGTGTATGTCAGTGTAGCTTTGTATTCTATTATTGAG
GCTAAAAGTTGATGTGTGACAAAATCTTATGTGTTGTATGTCAGTGTAAACATGCAGATGTA
TATTGCA GTTTGAAAGTGATCATTACTGTGGAATGCTAAAATACATTAATTCTAAAAC
CTGTGATGCCCTAAGAACATTAAGAACATGAAGGTGTTGACTAATAGAAACTAAGTACAGAA
AATTTCAGTTAGGTGGTTGAGCTGATGAGTTATTACCTCATAGAGACTATAATTCTA
TTGGTATTATATTGATGTTGCTGTTCTCAAACATTAAATCAAGCTTGGACTAA
TTATGCTAATTGAGTTCTGATCATTGAGCTCTGAAGCTTGAATCATTAGTGGT
GAGATGGCCTCTGGTAAGTGAATATTACCTCTGTAGGAAAAGGTGGAAAATAAGCATCTA
GAAGGTTGTTGTGAATGACTCTGTGCTGGCAAAATGCTTGAACACTCTATATTCTTCGT
TCATAAGAGGTAAAGGTCAAATTTCACAAAAGTCTTTAATAACAAAAGCATGCAGTTC
TCTGTGAAATCTCAAATATTGTTGAATAGTCTGTTCAATCTTAAAGAATCA

FIGURE 46

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96889
><subunit 1 of 1, 339 aa, 1 stop
><MW: 36975, pi: 7.85, NX(S/T): 1
MAAACGPGAAAGYCLLGLHLFLLTAGPALGWNDPDRMLLRDVKALTLYHYDRYTTSRRLDPIP
QLKCVGGTAGCDSYTPKVIQCQNKWDGYDVQWECKTDLDIAYKFGKTVSCEGYESSEDQY
VLRGSCGLEYNLDYTELGLQKLKESGKQHGFASFSDYYYKWSSADSCNMSGLITIVVLLGIA
FVVYKLFLSDGQYSPPPYSEYPPFSHRYQRFTNSAGPPPGFKSEFTGPQNTGHATSGFGS
AFTGQQGYENSGPGFWTGLGTGGILGYLFGSNRAATPFSDSWYYPSYPPSYPGTWNRAYSP
HGGSGSYSVCSNSDTKTRTASGYGGRRR
```

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 171-190

N-glycosylation site.

amino acids 172-176

Glycosaminoglycan attachment sites.

amino acids 244-248, 259-263, 331-335

Tyrosine kinase phosphorylation site.

amino acids 98-106

N-myristoylation sites.

amino acids 68-74, 69-75, 131-137, 241-247, 247-253, 266-272,
270-276, 278-284, 312-318